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EXPRESS MAIL NO.: EL668292918US **PATENT**
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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Weigel et al	Atty Dkt No:	5820.603
Serial No:	09/842,930		
Filed:	April 25, 2001		
For:	IDENTIFICATION AND USES OF A HYALURONAN RECEPTOR FOR ENDOCYTOSIS		

Box Missing Parts
Commissioner for Patents
Washington, D.C. 20231

PRELIMINARY AMENDMENT

Applicant herein seeks to amend the above referenced application as shown below, prior to the first examination and action of the United States Patent and Trademark Office, in response to the Notice to File Missing Parts of Nonprovisional Application mailed June 25, 2001.

In the Drawings:

Please accept the formal Drawings filed herewith.

In the Specification:

Please amend Tables III-V of the Specification (located on pages 94-96 of the Specification) as submitted on the following pages in clean, replacement form. Also, following the Remarks section are redline, marked-up versions of such tables illustrating the amendments made thereto.

Table III

Oligonucleotide Primers Used for RT-PCR Analysis and DNA Sequencing

Primer	SEQ ID NO:	Sequence	Position	PCR Product (bp)	Peptide Sequences confirmed
BAB1F	5	TCAATATAATCTGGCGAATGCAAT	3-26		
HSP2R	7	AGTTCCGAATGGGCAGGTCAGCTC	397-420	418	3
BAB3F	26	ATGAGGAAGCTCGGGTTAAAG	1452-1472		
BAB4R	29	GATGTAGCCATTGTTTGTTGCCAA	1769-1792	341	2
HSP2F	33	GAGCTGACCTGCCCATTCGGAACT	397-420		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	1076	4
BAB6F	30	AGACGCCAAATGTGTCGACCTCCA	3078-3101		
BAB7R	31	GAATAGGCCAGCACTTCCGTCAGG	3510-3533	456	2
BAB1F	5	TCAATATAATCTGGCGAATGCAAT	3-26		
BAB10R	32	GGTGAGGCAGTTGGCGCTGGTATG	851-874	872	3
HSP2F	33	GAGCTGACCTGCCCATTCGGAACT	397-420		
BAB10R	32	GGTGAGGCAGTTGGCGCTGGTATG	851-874	478	3
BAB10F	34	CATACCAGCGCCAACTGCCTCACC	851-874		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	622	3
BAB9F	36	CAAGTACGGCATCCACTGTGACCA	697-720		
HSP3R	35	CTTTAACCCGAGCTTCCTCAT	1452-1472	776	3

Other Primers used for RT-PCR and sequencing.

Name	SEQ ID NO:	Sequence	Position
5F	37	GGCTACTTCGGGCGAGACTGTCAG	2386-2409
5R	38	CTGACAGTCTCGCCCGAAGTAGCC	2386-2409
8F	39	TTGTACTCTTCAGCTGGCACC	4406-4426
8R	6	GGTGCCAGCTGAAGAGTACAA	4406-4426

Table IV

Summary of Amino Acid Sequences Derived From Peptides of the Purified Human 190 kDa HARE Protein

The human HARE proteins were immuno-affinity-purified from human spleen, subjected to SDS-PAGE and the 190 kDa protein band was excised and analyzed for internal peptide sequence following trypsin digestion. The amino acid sequences of these ten tryptic peptides were highly homologous or identical to the sequences of the rat 175 kDa HARE, reported herein above, and seven of these (not in bold face) were identical to regions within a human hypothetical protein of unknown expression and unknown function under GenBank accession number BAB15793. HARE peptides in boldface were not in the ORF for BAB15793.

Peptide Designation	Amino Acid Sequences	Start-End Residue	SEQ ID NO:
PR 1822	XSKPK	758-761	40
PR 1823	LTFDK	1054-1058	41
PR 1825-1st	GSIYQELPK	440-448	42
PR 1825-2nd	GTLFVPQNSGLGE	1198-1210	43
PR 1826	DLVGPGPFTVFAPLSAAFDEEAR	466-488	44
PR 1869-1st	**ELTSPFGTK**	**133-141**	45
PR 1869-2nd	MPQVLR	498-503	46
PR 1870	SPLGQYK	1047-1053	47
PR 1871-1st	**VLEIQK**	**107-112**	48
PR 1872	**VIHGLGK**	**100-106**	49

Table V

Molecular Mass Mapping of Peptides Derived From the Human 190 kDa HARE Protein

THE MOLECULAR MASSES OF SEVEN PEPTIDES DERIVED FROM TRYPTIC DIGESTION OF THE PURIFIED HUMAN 190 KDA HARE PROTEIN WERE DETERMINED BY MALDI-TOF MASS SPECTROMETRY AT THE LOUISIANA STATE UNIVERSITY PROTEIN CHEMISTRY FACILITY CORRESPONDED WITH PERFECT IDENTITY TO DEDUCED SEQUENCES WITHIN A PREDICTED HUMAN PROTEIN OF UNKNOWN FUNCTION (ACCESSION NUMBER BAB15793). THE MONOISOTOPIC PEPTIDE MASSES WERE SEARCHED AGAINST ENTRIES IN THE DATABASE, USING PEPTIDESEARCH SOFTWARE FROM THE EMBL PROTEIN AND PEPTIDE GROUP. IDENTICAL MASSES ARE ASSIGNED IN THIS SEARCH IF THE DIFFERENCE BETWEEN THE OBSERVED AND PREDICTED (CALCULATED) MASSES FOR A PEPTIDE IS < 0.2 DA. THE CORRESPONDING STARTING AND ENDING RESIDUES FOR EACH PEPTIDE WITHIN THE DEDUCED PROTEIN SEQUENCE IS SHOWN. THE N-TERMINAL R OR K RESIDUES IN PARENTHESES INDICATE THE DEDUCED RESIDUE IN THE PROTEIN AND CONFIRM THAT TRYPSIN DIGESTION OCCURRED ON THE C-TERMINAL SIDE OF THOSE AMINO ACIDS AS EXPECTED.

Measured Mass (Da)	Calculated Mass (Da)	Mass Difference (Da)	Start-End Residues	Sequence in Deduced Human	SEQ ID NO:
599.273	599.294	-0.021	796-800	(K)GYFGR	50
671.384	671.399	-0.015	656-660	(K)FHVIR	51
792.621	792.426	0.195	1047-1053	(R)SPLGQYK	52
1034.621	1034.552	0.068	440-448	(R)GSIYQELPK	53
1061.781	1061.584	0.196	677-686	(K)TLQGSELSVK	54
1624.051	1623.886	0.165	1047-1060	(R)SPLGQYKLTFDKAR	55
1092.771	1092.588	0.183	495-503	(K)YGLMPQVLR	56

In the Sequence Listing:

Please delete the Sequence Listing submitted on pages 139-207 of the Specification and substitute therefore the substitute Sequence Listing filed herewith under 37 CFR 1.825. The Sequence Listing filed with the application on April 25, 2001 did not contain a SEQ ID NO:37, and therefore the substitute Sequence Listing submitted herewith has been renumbered so that SEQ ID NOs:38-57 are now SEQ ID NOs:37-56. The Specification has been amended herein above to also reflect such renumbering of the SEQ ID NOs. In addition, the substitute Sequence Listing has been reformatted to fully comply with 37 CFR 1.821-1.823. The substitute Sequence Listing contains no new matter.

Also submitted herewith is a substitute copy of the Computer Readable Form of the substitute Sequence Listing under 37 CFR 1.825 which fully complies with the requirements of 37 CFR 1.821-1.824. The Computer Readable Form contains all previously submitted data with the above requested amendments incorporated therein. The copy of the Sequence Listing in Computer Readable Form is the same as the substitute copy of the Sequence Listing filed herewith.

REMARKS

This is meant to be a complete response to the Notice to File Missing Parts of NonProvisional Application mailed June 25, 2001. In the Notice to File Missing Parts, it was noted that the oath or declaration was missing. In addition, the application was considered informal since it does not comply with the regulations, and the required items identified below were required to be timely submitted to avoid abandonment:

(1) substitute drawings in compliance with 37 CFR 1.84 because the drawing sheets did not have the appropriate margins;

(2) a statement that the content of the sequence listing information recorded in computer readable form is identical to the written sequence listing and, where applicable, includes no new matter;

(3) a substitute computer readable form (CRF) copy of the Sequence Listing, as the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written sequence listing and, where applicable, includes no new matter.

In response to the Notice to File Missing Parts, submitted herewith are a properly signed oath/declaration in compliance with 37 CFR 1.63 and formal Drawings having the appropriate margins.

Also in response to the Notice to File Missing Parts, the Sequence Listing submitted on Pages 139-207 of the Specification and in Computer Readable Form, was reviewed. In addition to the fact that such copies of the Sequence Listing did not comply with the requirements of 37 CFR 1.822 and/or 1.823, as noted in the Notice to File Missing Parts, it was noted that no SEQ ID NO:37 appeared in the Sequence Listing or the disclosure contained in the Specification. Therefore, a substitute written copy of the Sequence Listing is submitted herewith in compliance with 37 CFR 1.825. Such substitute Sequence Listing has been amended to fully comply with 37 CFR 1.822 and 1.823, and SEQ ID NOs:38-57 have been renumbered as SEQ ID NOs:37-56. The substitute written copy of the Sequence Listing contains no new matter. In addition, a substitute copy of the Computer Readable Form of the Sequence Listing is submitted herewith which includes all previously submitted data and has been amended to fully comply with 37 CFR 1.822 and 1.823, and SEQ ID NOs:38-57 have been renumbered as SEQ ID NOs:37-56. The substitute copy of the Sequence Listing in computer readable form is identical to the substitute copy of the Sequence Listing in written form submitted herewith.

In addition, the Specification has been amended herein to renumber SEQ ID NOs:38-57 as SEQ ID NOs:37-56, for the reasons explained herein above in regards to the Sequence Listing. No substantive changes have been made in the application and such amendments do not introduce any new matter. Applicant respectfully requests that such amendments be entered into the

record.

Should the Examiner have any questions or comments concerning the before-mentioned amendments to the application or any other matter, Applicant's agent will welcome the opportunity to discuss same with the Examiner.

Respectfully submitted,

Kathryn L. Hester, Ph.D.
Registration No. 46,768
DUNLAP, CODDING & ROGERS, P.C.
9400 N. Broadway, Suite 420
Oklahoma City, Oklahoma 73114
(405) 478-5344

Agent for Applicant

MARKED-UP VERSION OF THE PARAGRAPHS OF THE SPECIFICATION

SHOWING THE CHANGES MADE THERETO

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PR 1872	**VIHGLGK**	**100-106**	[50] 49

Table V

Molecular Mass Mapping of Peptides Derived From the Human 190 kDa HARE Protein

The molecular masses of seven peptides derived from tryptic digestion of the purified human 190 kDa HARE protein were determined by MALDI-TOF mass spectrometry at the Louisiana State University Protein Chemistry Facility corresponded with perfect identity to deduced sequences within a predicted human protein of unknown function (accession number BAB15793). The monoisotopic peptide masses were searched against entries in the database, using PeptideSearch software from the EMBL Protein and Peptide Group. Identical masses are assigned in this search if the difference between the observed and predicted (calculated) masses for a peptide is < 0.2 Da. The corresponding starting and ending residues for each peptide within the deduced protein sequence is shown. The N-terminal R or K residues in parentheses indicate the deduced residue in the protein and confirm that trypsin digestion occurred on the C-terminal side of those amino acids as expected.

Measured Mass (Da)	Calculated Mass (Da)	Mass Difference (Da)	Start-End Residues	Sequence in Deduced Human	SEQ ID NO:
599.273	599.294	-0.021	796-800	(K)GYFGR	[51] 50
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